

032301.213.seq.ST25.txt
SEQUENCE LISTING

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<110> Farwick, Mike
<120> NUCLEOTIDE SEQUENCES CODING FOR THEpstC2 GENE
<130> 032301W213
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<170> PatentIn version 3.1
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<211> 1540
<212> DNA
<213> Corynebacterium glutamicum
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<222> (230)..(1294)
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032301.213.seq.ST25.txt

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Leu Leu Ala Ala Thr Leu Leu Ile Ser Val Ile Ala Leu Ile Ile Ala
120 125 130

622

atg ccc att gct ctt ggt att gcg atc ttc ttg tcc aac tac tca cca
Met Pro Ile Ala Leu Gly Ile Ala Ile Phe Leu Ser Asn Tyr Ser Pro
135 140 145

670

aaq cgc ctc gtt aag cca ctt ggc tac atg gtg gac atg ctg gct gct
Lys Arg Leu Val Lys Pro Leu Gly Tyr Met Val Asp Met Leu Ala Ala
150 155 160

718

gtg cct tcc atc gtc tac ggc ctt tgg ggc tgg cag gtg ctc gga cca
Val Pro Ser Ile Val Tyr Gly Leu Trp Gly Trp Gln Val Leu Gly Pro
165 170 175

766

gtt ctg tcc ggt ttc tac acc tgg att gaa aac tgg gtc ggt ggc aac ttc
Ala Leu Ser Gly Phe Tyr Thr Trp Ile Glu Ser Trp Gly Gly Ser Phe
180 185 190 195

814

tcc ctc ttc gct act tac caa aac tca cct tct ttt gct acc ggc cgt
Phe Leu Pro Ala Thr Tyr Gln Asn Ser Pro Ser Phe Ala Thr Gly Arg
200 205 210

862

aac atg ctc acc ggt ggc atc gtg ctc gca gtg atg atc ctt cct gtt
Asn Met Leu Thr Gly Ile Val Leu Ala Val Met Ile Leu Pro Val
215 220 225

910

atc gca gca aac gca cgt gaa gtt ttc ata cag act cca aag ggc cac
Ile Ala Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro Lys Gly His
230 235 240

958

atc gaa tcc gtc act ctt gca ctt ggc gca aac cgc tgg gaa gtc gtt cgt
Ile Glu Ser Ala Leu Ala Leu Gly Ala Thr Arg Trp Glu Val Val Arg
245 250 255

1006

tcc aca gtt ctc cca ttc gga atg tcc ggc tac gtc gtt tcc ggc gcg atg
Leu Thr Val Leu Pro Phe Gly Met Ser Gly Tyr Val Ser Gly Ala Met
260 265 270 275

1054

ctc ggc ctc ggc cgc gca ctg ggt gag acc atg gcg cta tac atg gtt
Leu Gly Leu Gly Arg Ala Leu Gly Glu Thr Met Ala Leu Tyr Met Val
280 285 290

1102

gtt tcc cca tcc tcc ggg ttc cgc ttc tcc gtt ggt ggc ggt acc
Val Ser Pro Ser Ser Ala Phe Arg Phe Ser Leu Phe Asp Gly Gly Thr
295 300 305

1150

acc ttc gca aac gca atc gca aat gca gtc gct cca gaa ttc aac gac aac
Thr Phe Ala Thr Ala Ile Ala Asn Ala Ala Pro Glu Phe Asn Asp Asn
310 315 320

1198

acc cgc gca ggc ggg tcc atc tcc gca ggc ctc gtg ctg ttc gca ctt
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325 330 335

1246

032301.213.seq.ST25.txt
acc ttc atc gtc aac gct ggc gct cgc gcc atg gtt aac cgc gga aag 1294
Thr Ile Val Asn Ala Gly Ala Arg Ala Met Val Asn Arg Gly Lys
340 345 350 355

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cgtaatccat	tatggtgccg	tgcctatcgc	agctgtgcac	ctggtttggg	tgcgtgtggac	1474
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Lys Pro Ser Lys Lys Ile Val Ala Glu Gly Gly Gly Ser Val Lys Arg
 35 40 45

Pro Gly Asp Arg Ile Phe Glu Val Leu Ser Thr Ala Ser Ala Ala Ile
 50 55 60

110 Thr Ala Ile Ile Ile Ile Ala Ala Ala Phe Leu Ile Trp Arg Ala
65 70 75 80

Val Pro Ala Leu Met Arg Asn Ala Glu Gly Ile Gly Gly Phe Phe Thr
 85 90 95

Tyr Ser Gly Ala Trp Asn Thr Thr Asp Ile Asp Ala Met Tyr Phe Gly
 100 105 110

Ile Pro Asn Leu Leu Ala Ala Thr Leu Leu Ile Ser Val Ile Ala Leu
 115 120 125

Ile Ile Ala Met Pro Ile Ala Leu Gly Ile Ala Ile Phe Leu Ser Asn
130 135 140

Tyc Ser Pro Lys Arg Lys Val Lys Pro Leu Gly Tyr Met Val Asp Met
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145 150 155 160

Leu Ala Ala Val Pro Ser Ile Val Tyr Gly Leu Trp Gly Trp Gln Val
165 170 175

Ileu Gly Pro Ala Leu Ser Gly Phe Tyr Thr Trp Ile Glu Ser Trp Gly
180 185 190

Gly Ser Phe Phe Leu Phe Ala Thr Tyr Gln Asn Ser Pro Ser Phe Ala
195 200 205

Thr Gly Arg Asn Met Leu Thr Gly Gly Ile Val Leu Ala Val Met Ile
210 215 220

Leu Pro Val Ile Ala Ala Thr Ala Arg Glu Val Phe Ile Gln Thr Pro
225 230 235 240

Lys Gly His Ile Glu Ser Ala Leu Ala Leu Gly Ala Thr Arg Trp Glu
245 250 255

Val Val Arg Leu Thr Val Leu Pro Phe Gly Met Ser Gly Tyr Val Ser
260 265 270

Gly Ala Met Leu Gly Leu Gly Arg Ala Leu Gly Glu Thr Met Ala Leu
275 280 285

Tyr Met Val Val Ser Pro Ser Ser Ala Phe Arg Phe Ser Leu Phe Asp
290 295 300

Gly Gly Thr Thr Phe Ala Thr Ala Ile Ala Asn Ala Ala Pro Glu Phe
305 310 315 320

Asn Asp Asn Thr Arg Ala Gly Ala Tyr Ile Ser Ala Gly Leu Val Leu
325 330 335

Phe Ala Leu Thr Phe Ile Val Asn Ala Gly Ala Arg Ala Met Val Asn
340 345 350

Arg Gly Lys
355